

SEQUENCE LISTING

<110> Hu, Xu
Lu, Guihua

<120> Pathogen-Responsive Genes, Promoters,
Regulatory Elements and Methods of Use for Same

<130> 1469

<150> 60/414,771

<151> 2002-09-30

<160> 34

<170> FastSEQ for Windows Version 4.0

<210> 1

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<222> (370)...(1620)

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aagcacattc gcgcgctgct cgcccgccgc cacggttccg tcaagccgaa cgaagcctcc 180
ataccggagg ccagcgagtg tgagctcggc ctcgacaaga gctttggctt tgctaagcag 240
ttttcggctc attatgagct cagtgcgaa gtcggccggg ggcatttttg gtatacctgc 300
tccgctaaag gcaagaaagg ggcgttcaag ggcttaaagt ttgctgtcaa agtcattcct 360
aaagccaag atg acc aca gca att gct ata gag gat gta agg aga gaa gtg 411
Met Thr Thr Ala Ile Ala Ile Glu Asp Val Arg Arg Glu Val
1 5 10
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Lys Ile Leu Arg Ala Leu Thr Gly His Lys Asn Leu Val Gln Phe Tyr
15 20 25 30
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Glu Ala Tyr Glu Asp Asp Asp Asn Val Tyr Ile Val Met Glu Leu Cys
35 40 45
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aaa gga ggg gaa ttg cta gat agg att ctt tcc agg ggt gga aag tac 555
Lys Gly Gly Glu Leu Leu Asp Arg Ile Leu Ser Arg Gly Gly Lys Tyr
50 55 60
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tca gaa gag gat gcc aga gta gtt atg atc caa ata ttg agt gtg gta 603
Ser Glu Glu Asp Ala Arg Val Val Met Ile Gln Ile Leu Ser Val Val
65 70 75
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gct ttt tgt cat ctg cag ggt gtt gtt cac cgt gat ctc aag cca gag 651
Ala Phe Cys His Leu Gln Gly Val Val His Arg Asp Leu Lys Pro Glu
80 85 90
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Asn Phe Leu Phe Thr Ser Lys Asp Asp Lys Ser Thr Leu Lys Ala Ile	
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gat ttt ggg ttg tct gac tat gta aag cca gat gag agg ttg aat gat	747
Asp Phe Gly Leu Ser Asp Tyr Val Lys Pro Asp Glu Arg Leu Asn Asp	
115 120 125	
att gtg gga agt gct tat tat gta gct cca gaa gtt ttg cat aga tct	795
Ile Val Gly Ser Ala Tyr Tyr Val Ala Pro Glu Val Leu His Arg Ser	
130 135 140	
tat ggg aca gag gca gat atg tgg agc att ggt gta att gct tat att	843
Tyr Gly Thr Glu Ala Asp Met Trp Ser Ile Gly Val Ile Ala Tyr Ile	
145 150 155	
ctt tta tgc gga agc cgt ccc ttt tgg gcc cgg aca gaa tct ggt ata	891
Leu Leu Cys Gly Ser Arg Pro Phe Trp Ala Arg Thr Glu Ser Gly Ile	
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Phe Arg Ala Val Leu Lys Ala Asp Pro Ser Phe Asp Glu Ala Pro Trp	
175 180 185 190	
cct tct tta tcg gtt gat gcc aaa gat ttt gta aag agg ttg ttg aat	987
Pro Ser Leu Ser Val Asp Ala Lys Asp Phe Val Lys Arg Leu Leu Asn	
195 200 205	
aag gat tat cgt aaa aga ttg act gcg gct cag gca cta agt cat cca	1035
Lys Asp Tyr Arg Lys Arg Leu Thr Ala Ala Gln Ala Leu Ser His Pro	
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tgg ctg gtg aat cat cat gat gat atg agg ata cct ttg gat atg ata	1083
Trp Leu Val Asn His His Asp Asp Met Arg Ile Pro Leu Asp Met Ile	
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atc cac aag ctt gtt aaa gct tac att tgc tcg tct tcg ttg cgc aaa	1131
Ile His Lys Leu Val Lys Ala Tyr Ile Cys Ser Ser Ser Leu Arg Lys	
240 245 250	
tct gct tta cgg gct ctt gca aag aca tta aca gta gct cag cta gct	1179
Ser Ala Leu Arg Ala Leu Ala Lys Thr Leu Thr Val Ala Gln Leu Ala	
255 260 265 270	
tat ctc aga gat caa ttt act ctg tta ggg cca aac aaa agt gga tta	1227
Tyr Leu Arg Asp Gln Phe Thr Leu Leu Gly Pro Asn Lys Ser Gly Leu	
275 280 285	
att tct atg cag aac ttt aag acg gct gtt ttg agg agc tct aca gat	1275
Ile Ser Met Gln Asn Phe Lys Thr Ala Val Leu Arg Ser Ser Thr Asp	
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gcc tca aag gat tca cgg gtc tta gat tat gtc agt atg gtt agt tct	1323
Ala Ser Lys Asp Ser Arg Val Leu Asp Tyr Val Ser Met Val Ser Ser	
305 310 315	
atc caa tat agg aaa tta gat ttt gag gag ttt tgt gct gct gct ata	1371

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Ile Gln Tyr Arg Lys Leu Asp Phe Glu Glu Phe Cys Ala Ala Ala Ile
 320                      325                      330

agt gtg cac caa ctc gag gga atg gag acc tgg gag caa cat gca agg 1419
Ser Val His Gln Leu Glu Gly Met Glu Thr Trp Glu Gln His Ala Arg
335                      340                      345                      350

cat gcc tat gag ctt ttt aaa aag gaa gga aat aga cca att atg att 1467
His Ala Tyr Glu Leu Phe Lys Lys Glu Gly Asn Arg Pro Ile Met Ile
                      355                      360                      365

gaa gaa ctt gcc tcg gaa ctt ggg ctt agt cca tca gta cct gtt cat 1515
Glu Glu Leu Ala Ser Glu Leu Gly Leu Ser Pro Ser Val Pro Val His
                      370                      375                      380

gta gta ctt cag gat tgg ata agg cac tca gat gga aag ctt agt ttc 1563
Val Val Leu Gln Asp Trp Ile Arg His Ser Asp Gly Lys Leu Ser Phe
                      385                      390                      395

ttg gga ttt gtc agg ctt ctg cat ggg gtt tct tcc cgc gca ttt cag 1611
Leu Gly Phe Val Arg Leu Leu His Gly Val Ser Ser Arg Ala Phe Gln
400                      405                      410

aag gct tga gagaatgtac acacagttgc tattatTTTT tcttgcccgt 1660
Lys Ala *
415

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tacctttaaa tattttgatg gtacctaaat gcatgagcta actccatcag cagacctcag 1720
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catatatcta tcccactttt ccaagattta caaacacaaac ctatatccc caccttgttt 1840
ctcactcact ttagtttggg ggttctggag ttagaagctt gtacagttga aagctagacc 1900
aaaaattgta cccaccttgt ctttaagggtt tacccttgt gtacccatgg cacctatcaa 1960
taaacatcac gtgaactcct tgataataga cagatatgta gccttttttt cgtagtattt 2020
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aacttctaac gatatcagtg taaagttttg cttttgaaga cattcaaaag cttctggagt 2260
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<212> PRT
<213> Glycine max

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 20          25          30
Tyr Glu Asp Asp Asn Val Tyr Ile Val Met Glu Leu Cys Lys Gly
 35          40          45
Gly Glu Leu Leu Asp Arg Ile Leu Ser Arg Gly Gly Lys Tyr Ser Glu
 50          55          60
Glu Asp Ala Arg Val Val Met Ile Gln Ile Leu Ser Val Val Ala Phe
 65          70          75          80
Cys His Leu Gln Gly Val Val His Arg Asp Leu Lys Pro Glu Asn Phe
 85          90          95

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10					15					20						
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Arg	Gln	Ala	Ala	Lys	Leu	Thr	Lys	Thr	Ile	Val	Gly	Val	Val	Glu	Ala	
		25						30					35			
tgc	cat	tct	ctt	ggt	gtg	atg	cac	aga	gac	ctt	aaa	cct	gag	aat	ttt	199
Cys	His	Ser	Leu	Gly	Val	Met	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn	Phe	
		40					45					50				
ctc	ttt	gtc	aat	cag	cac	gag	gat	tcc	ctt	ctc	aaa	acc	att	gac	ttt	247
Leu	Phe	Val	Asn	Gln	His	Glu	Asp	Ser	Leu	Leu	Lys	Thr	Ile	Asp	Phe	
	55					60					65					
gga	tta	tct	gtc	ttc	ttt	aag	cca	ggt	gat	ata	ttt	aat	gat	gtg	gtg	295
Gly	Leu	Ser	Val	Phe	Phe	Lys	Pro	Gly	Asp	Ile	Phe	Asn	Asp	Val	Val	
	70				75					80					85	
ggc	agc	cca	tac	tat	gtt	gcc	ccg	gat	gtt	ttg	cga	aag	cgt	tat	ggt	343
Gly	Ser	Pro	Tyr	Tyr	Val	Ala	Pro	Asp	Val	Leu	Arg	Lys	Arg	Tyr	Gly	
			90						95					100		
cct	gag	gca	gat	gtt	tgg	agt	gct	ggt	gtt	atc	ctt	tac	att	ctt	ttg	391
Pro	Glu	Ala	Asp	Val	Trp	Ser	Ala	Gly	Val	Ile	Leu	Tyr	Ile	Leu	Leu	
			105					110					115			
agt	gga	gta	cct	cca	ttt	tgg	gct	gaa	aac	gaa	caa	gga	ata	ttt	gaa	439
Ser	Gly	Val	Pro	Pro	Phe	Trp	Ala	Glu	Asn	Glu	Gln	Gly	Ile	Phe	Glu	
		120					125					130				
caa	gtt	ctg	cgt	ggt	gat	ctt	gac	ttt	tct	tct	gat	ccc	tgg	cct	tca	487
Gln	Val	Leu	Arg	Gly	Asp	Leu	Asp	Phe	Ser	Ser	Asp	Pro	Trp	Pro	Ser	
	135					140					145					
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Ile	Ser	Glu	Ser	Ala	Lys	Asp	Leu	Val	Arg	Lys	Met	Leu	Val	Arg	Asp	
	150				155					160					165	
cct	aga	agg	cgg	ttg	act	gca	cat	caa	gta	tta	tgt	cat	cct	tgg	att	583
Pro	Arg	Arg	Arg	Leu	Thr	Ala	His	Gln	Val	Leu	Cys	His	Pro	Trp	Ile	
				170					175					180		
caa	gtt	gat	ggt	gta	gct	cct	gac	aag	cca	ctt	gat	tct	gcc	gta	tta	631
Gln	Val	Asp	Gly	Val	Ala	Pro	Asp	Lys	Pro	Leu	Asp	Ser	Ala	Val	Leu	
			185					190					195			
agt	cgc	ttg	aag	caa	ttt	tct	gct	atg	aac	aag	ctc	aaa	aaa	atg	gcc	679
Ser	Arg	Leu	Lys	Gln	Phe	Ser	Ala	Met	Asn	Lys	Leu	Lys	Lys	Met	Ala	
		200					205					210				
ctt	ata	att	att	gca	gag	agc	tta	tct	gaa	gaa	gaa	ata	gct	ggc	tta	727
Leu	Ile	Ile	Ile	Ala	Glu	Ser	Leu	Ser	Glu	Glu	Glu	Ile	Ala	Gly	Leu	
	215					220					225					
aaa	gaa	atg	ttc	aag	atg	ata	gat	gca	gat	aac	agt	ggt	caa	atc	act	775
Lys	Glu	Met	Phe	Lys	Met	Ile	Asp	Ala	Asp	Asn	Ser	Gly	Gln	Ile	Thr	
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ttt gaa gaa ctt aaa gct ggt ttg aaa aga gtc ggc gct aat ctt aag 823
Phe Glu Glu Leu Lys Ala Gly Leu Lys Arg Val Gly Ala Asn Leu Lys
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gag tct gaa att tat gat tta atg caa gca gct gat gtt gat aac agt 871
Glu Ser Glu Ile Tyr Asp Leu Met Gln Ala Ala Asp Val Asp Asn Ser
      265      270      275

ggg aca att gat tac ggc gag ttc ctt gct gca acg ttg cac cgc aac 919
Gly Thr Ile Asp Tyr Gly Glu Phe Leu Ala Ala Thr Leu His Arg Asn
      280      285      290

aaa att gaa aga gaa gat aat cta ttt gca gcc ttt tct tac ttt gat 967
Lys Ile Glu Arg Glu Asp Asn Leu Phe Ala Ala Phe Ser Tyr Phe Asp
      295      300      305

aaa gat gga agt ggc tat att act cag gaa gaa ctt caa cag gct tgt 1015
Lys Asp Gly Ser Gly Tyr Ile Thr Gln Glu Glu Leu Gln Gln Ala Cys
310      315      320

gat gag ttt ggc ata aaa gat gtc cgt ttg gaa gag ata atc aag gaa 1063
Asp Glu Phe Gly Ile Lys Asp Val Arg Leu Glu Glu Ile Ile Lys Glu
      330      335      340

att gat gaa gat aat gat gga cgc ata gat tac aat gag ttt gtg gct 1111
Ile Asp Glu Asp Asn Asp Gly Arg Ile Asp Tyr Asn Glu Phe Val Ala
      345      350      355

atg atg cag aaa gga aat ctt cca gcg gtt ggt aag aag ggc cta gaa 1159
Met Met Gln Lys Gly Asn Leu Pro Ala Val Gly Lys Lys Gly Leu Glu
      360      365      370

aat agc ttc agc gtt aag ttc agg gag gca tta aaa ttg tag 1201
Asn Ser Phe Ser Val Lys Phe Arg Glu Ala Leu Lys Leu *
      375      380      385

ttttcattgt catcattgag tttttttttt ttttttggtg ctcttttatta ccacacatcc 1261
ctcctttttca ctttgaaggt tcaagatttt attcatagtg caaagtgttt gcatggggat 1321
atntaggtgg gcctttttcat ctctgcagtt attttgtttg cgtccaattt aaaatggatt 1381
tttghtaatta cgagaatata ttaaaaagag atatcttttt ttattattat attaaaaaga 1441
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taaaaaaaaaa aaaaaaaaaa 1520

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<211> 386
<212> PRT
<213> Glycine max

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20     25     30
Gly Val Val Glu Ala Cys His Ser Leu Gly Val Met His Arg Asp Leu
35     40     45
Lys Pro Glu Asn Phe Leu Phe Val Asn Gln His Glu Asp Ser Leu Leu
50     55     60
Lys Thr Ile Asp Phe Gly Leu Ser Val Phe Phe Lys Pro Gly Asp Ile

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65					70					75					80
Phe	Asn	Asp	Val	Val	Gly	Ser	Pro	Tyr	Tyr	Val	Ala	Pro	Asp	Val	Leu
				85					90					95	
Arg	Lys	Arg	Tyr	Gly	Pro	Glu	Ala	Asp	Val	Trp	Ser	Ala	Gly	Val	Ile
			100					105					110		
Leu	Tyr	Ile	Leu	Leu	Ser	Gly	Val	Pro	Pro	Phe	Trp	Ala	Glu	Asn	Glu
		115					120					125			
Gln	Gly	Ile	Phe	Glu	Gln	Val	Leu	Arg	Gly	Asp	Leu	Asp	Phe	Ser	Ser
	130					135					140				
Asp	Pro	Trp	Pro	Ser	Ile	Ser	Glu	Ser	Ala	Lys	Asp	Leu	Val	Arg	Lys
145					150					155					160
Met	Leu	Val	Arg	Asp	Pro	Arg	Arg	Arg	Leu	Thr	Ala	His	Gln	Val	Leu
				165					170					175	
Cys	His	Pro	Trp	Ile	Gln	Val	Asp	Gly	Val	Ala	Pro	Asp	Lys	Pro	Leu
			180					185					190		
Asp	Ser	Ala	Val	Leu	Ser	Arg	Leu	Lys	Gln	Phe	Ser	Ala	Met	Asn	Lys
	195						200					205			
Leu	Lys	Lys	Met	Ala	Leu	Ile	Ile	Ile	Ala	Glu	Ser	Leu	Ser	Glu	Glu
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Glu	Ile	Ala	Gly	Leu	Lys	Glu	Met	Phe	Lys	Met	Ile	Asp	Ala	Asp	Asn
225					230					235					240
Ser	Gly	Gln	Ile	Thr	Phe	Glu	Glu	Leu	Lys	Ala	Gly	Leu	Lys	Arg	Val
				245					250					255	
Gly	Ala	Asn	Leu	Lys	Glu	Ser	Glu	Ile	Tyr	Asp	Leu	Met	Gln	Ala	Ala
			260					265					270		
Asp	Val	Asp	Asn	Ser	Gly	Thr	Ile	Asp	Tyr	Gly	Glu	Phe	Leu	Ala	Ala
	275						280					285			
Thr	Leu	His	Arg	Asn	Lys	Ile	Glu	Arg	Glu	Asp	Asn	Leu	Phe	Ala	Ala
	290				295						300				
Phe	Ser	Tyr	Phe	Asp	Lys	Asp	Gly	Ser	Gly	Tyr	Ile	Thr	Gln	Glu	Glu
305					310					315					320
Leu	Gln	Gln	Ala	Cys	Asp	Glu	Phe	Gly	Ile	Lys	Asp	Val	Arg	Leu	Glu
				325					330					335	
Glu	Ile	Ile	Lys	Glu	Ile	Asp	Glu	Asp	Asn	Asp	Gly	Arg	Ile	Asp	Tyr
			340				345					350			
Asn	Glu	Phe	Val	Ala	Met	Met	Gln	Lys	Gly	Asn	Leu	Pro	Ala	Val	Gly
	355						360				365				
Lys	Lys	Gly	Leu	Glu	Asn	Ser	Phe	Ser	Val	Lys	Phe	Arg	Glu	Ala	Leu
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Lys	Leu														
385															

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 <213> Glycine max

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 gaactctgac atgttactct tcttcattct cttgagtgc aagaaattgc tttgaatggg 180
 tttttcatgg gatgtrtaga atccccctcc ttcacacact tgtttgatta caatatttgc 240
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 gtttttagag aagctgttgc tccgtgggat aaagaagtta tatccgaccc cagcacaccc 420
 aagcctaacc cagatccatt tttatacatt cctgaaggaa attctgatgt gagttttttt 480
 ctcccaccac tgaaaacttg gatctcccta tgttatatgc tgtgattaaa ttagttgtat 540

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ttctcttggtg ctacagcatt attttgaaat gcaagatggg gttattcgtg tatatccaga 600
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aggtggggtatc ttatgcatgc ttgcctatta cttgcagcaa aagaagagct ttttcctgta 720
gctgatgcaa ctacatttyt cacygatctt catcacttac ttcgagtcac agcagcaggg 780
aatataagaa ctttatgcca tcataggctc aatcttctag aacaagtaca tctctaattt 840
actgaaacaa actgcagcct atgcttgtat tttaattaca tacaagaatc aattgttgtt 900
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<222> (72)...(746)

<400> 6

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          Met Cys Gly Gly Ala Ile Ile Ser Asp Phe Ile Gly Val
              1              5              10

aag cgt ggc cgc aac ctc gcc gcg cag gaa ctg tgg tcc gag ctt gac 158
Lys Arg Gly Arg Asn Leu Ala Ala Gln Glu Leu Trp Ser Glu Leu Asp
      15              20              25

cct ttc tct gac ctc ctt ggc ttc gac acc acc acc acc acc acc acc 206
Pro Phe Ser Asp Leu Leu Gly Phe Asp Thr Thr Thr Thr Thr Thr Thr
      30              35              40              45

aac caa cca ccc ctt cca gac aaa aaa gtg gtg tca tca tgt gag aag 254
Asn Gln Pro Pro Leu Pro Asp Lys Lys Val Val Ser Ser Cys Glu Lys
              50              55              60

aag aag aag aaa agt gtg agt gca gaa aag aag agt ggt ggg cga gct 302
Lys Lys Lys Lys Ser Val Ser Ala Glu Lys Lys Ser Gly Gly Arg Ala
              65              70              75

cgg aag aac gtg tac aga gga atc agg caa agg ccg tgg ggc aag tgg 350
Arg Lys Asn Val Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp
              80              85              90

gcc gcg gaa ata agg gac cca cat aag ggc gtc cgc gtc tgg ctc ggc 398
Ala Ala Glu Ile Arg Asp Pro His Lys Gly Val Arg Val Trp Leu Gly
              95              100              105

acc ttc ccc acc gcc gag gaa gcc gcc cga gcc tac gac gac gcc gcc 446
Thr Phe Pro Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Asp Ala Ala
      110              115              120              125

aag cgc atc cgc ggc gac aag gcc aag ctc aac ttc ccg gcc acc gct 494
Lys Arg Ile Arg Gly Asp Lys Ala Lys Leu Asn Phe Pro Ala Thr Ala
              130              135              140

ccg cca ccc tcc aaa aaa caa cgc tgc ctc agc cct gac acc acc acc 542
Pro Pro Pro Ser Lys Lys Gln Arg Cys Leu Ser Pro Asp Thr Thr Thr
              145              150              155

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gaa caa agc agc agc tca caa tcc acc act gga tcc acc gga tcg ccg 590
 Glu Gln Ser Ser Ser Ser Gln Ser Thr Thr Gly Ser Thr Gly Ser Pro
 160 165 170

cct tcc gcc gcc ttc cac ggc gga gga gat gaa ctc gac ctg aaa caa 638
 Pro Ser Ala Ala Phe His Gly Gly Gly Asp Glu Leu Asp Leu Lys Gln
 175 180 185

ctt gaa cgg ttt cta ggg ttg gac aac atg ggt gct gag tgg gac aac 686
 Leu Glu Arg Phe Leu Gly Leu Asp Asn Met Gly Ala Glu Trp Asp Asn
 190 195 200 205

atg gat gac ctg tgg atg ctg gac gac gtc gtt gtg ccc aac cgt cac 734
 Met Asp Asp Leu Trp Met Leu Asp Asp Val Val Val Pro Asn Arg His
 210 215 220

tta att tac tag aaggagagata attaattaat taataaatgg cgttttctta 786
 Leu Ile Tyr *

agttatagtt ttataaaaact atgttggtgt atgtgttctt agttttctgt tttgtcttgt 846
 cctctcgctt tggtaatctt tgttttgtac ggtcgaatga tttcaaaatt atgtgcaacg 906
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 Asp Leu Leu Gly Phe Asp Thr Thr Thr Thr Thr Thr Asn Gln Pro
 35 40 45
 Pro Leu Pro Asp Lys Lys Val Val Ser Ser Cys Glu Lys Lys Lys Lys
 50 55 60
 Lys Ser Val Ser Ala Glu Lys Lys Ser Gly Gly Arg Ala Arg Lys Asn
 65 70 75 80
 Val Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu
 85 90 95
 Ile Arg Asp Pro His Lys Gly Val Arg Val Trp Leu Gly Thr Phe Pro
 100 105 110
 Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Asp Ala Ala Lys Arg Ile
 115 120 125
 Arg Gly Asp Lys Ala Lys Leu Asn Phe Pro Ala Thr Ala Pro Pro Pro
 130 135 140
 Ser Lys Lys Gln Arg Cys Leu Ser Pro Asp Thr Thr Thr Glu Gln Ser
 145 150 155 160
 Ser Ser Ser Gln Ser Thr Thr Gly Ser Thr Gly Ser Pro Pro Ser Ala
 165 170 175
 Ala Phe His Gly Gly Gly Asp Glu Leu Asp Leu Lys Gln Leu Glu Arg
 180 185 190
 Phe Leu Gly Leu Asp Asn Met Gly Ala Glu Trp Asp Asn Met Asp Asp
 195 200 205

Leu Trp Met Leu Asp Asp Val Val Val Pro Asn Arg His Leu Ile Tyr
 210 215 220

<210> 8
 <211> 969
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (49)...(762)

<400> 8
 agtaactctc tatttctctt tccatctctc aagttctgaa gaagaaac atg tgt gga 57
 Met Cys Gly
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ggt gct atc atc tca gac ttc att ggt gtg aag cgt ggc cgc aac ctc 105
 Gly Ala Ile Ile Ser Asp Phe Ile Gly Val Lys Arg Gly Arg Asn Leu
 5 10 15

gcc gcg cag gaa cta tgg tct gag ctt gac cct ttc tct gac ttc ctt 153
 Ala Ala Gln Glu Leu Trp Ser Glu Leu Asp Pro Phe Ser Asp Phe Leu
 20 25 30 35

ggc ttc gat acc acc aat tcc aaa aac caa cca ccc ctg cag aaa att 201
 Gly Phe Asp Thr Thr Asn Ser Lys Asn Gln Pro Pro Leu Gln Lys Ile
 40 45 50

cca gac aaa aaa gtg gtg tca tca tgt gag aag aag aag aaa agc gtg 249
 Pro Asp Lys Lys Val Val Ser Ser Cys Glu Lys Lys Lys Lys Ser Val
 55 60 65

gtg ggt gca gaa aag aag aag agt gat agt ggg cga gct cgt aaa aac 297
 Val Gly Ala Glu Lys Lys Lys Ser Asp Ser Gly Arg Ala Arg Lys Asn
 70 75 80

gtg tac aga gga atc agg caa agg cca tgg ggc aag tgg gcc gcg gag 345
 Val Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp Ala Ala Glu
 85 90 95

ata agg gac cca cac aag ggt gtt cgt gtc tgg ctc ggc acc ttc ccc 393
 Ile Arg Asp Pro His Lys Gly Val Arg Val Trp Leu Gly Thr Phe Pro
 100 105 110 115

acc gcc gaa gaa gcc gcc caa gcc tac gac gac gcc gcc ata cgc atc 441
 Thr Ala Glu Glu Ala Ala Gln Ala Tyr Asp Asp Ala Ala Ile Arg Ile
 120 125 130

cgc ggc gac aag gcc aag ctc aac ttc ccg gcc acc acc att tcc gcc 489
 Arg Gly Asp Lys Ala Lys Leu Asn Phe Pro Ala Thr Thr Ile Ser Ala
 135 140 145

gcc gcc gct ccg cca cct tcc aaa aag caa cgc tgc ctc agc cct gac 537
 Ala Ala Ala Pro Pro Pro Ser Lys Lys Gln Arg Cys Leu Ser Pro Asp
 150 155 160

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atc atc act gaa gaa agc agc agc agc agc tca cat tcc acc act gga 585
Ile Ile Thr Glu Glu Ser Ser Ser Ser Ser Ser His Ser Thr Thr Gly
165 170 175

tcc acc ggc gaa agc ggc gga gga aac gac gaa ctc gac ctg aaa caa 633
Ser Thr Gly Glu Ser Gly Gly Gly Asn Asp Glu Leu Asp Leu Lys Gln
180 185 190 195

att gaa tgg ttt cta ggt ttg gag aat gag ctg cct gtt agc aac aac 681
Ile Glu Trp Phe Leu Gly Leu Glu Asn Glu Leu Pro Val Ser Asn Asn
200 205 210

att ggt gct gag tgg gac aac atg gat gac ctg tgg atg ctg gac gac 729
Ile Gly Ala Glu Trp Asp Asn Met Asp Asp Leu Trp Met Leu Asp Asp
215 220 225

gtc gtt gtg ccc aac cgt cac tta att tac tag aaggctaata attaataaat 782
Val Val Val Pro Asn Arg His Leu Ile Tyr *
230 235

ggcgttttct taagtcttag ttttacttta taaattgtag tataaaacta tggttggtatt 842
tgtgttctta gttttcttct gctgttttgt ctcttctctg gctttggttaa tttctgtttt 902
ggacggttga atgatttcaa aattaggtac ttaattacac cctatcaaaa aaaaaaaaaa 962
aaaaaaa 969

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<210> 9
<211> 237
<212> PRT
<213> Glycine max

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Arg Asn Leu Ala Gln Glu Leu Trp Ser Glu Leu Asp Pro Phe Ser
20 25 30
Asp Phe Leu Gly Phe Asp Thr Thr Asn Ser Lys Asn Gln Pro Pro Leu
35 40 45
Gln Lys Ile Pro Asp Lys Lys Val Val Ser Ser Cys Glu Lys Lys Lys
50 55 60
Lys Ser Val Val Gly Ala Glu Lys Lys Lys Ser Asp Ser Gly Arg Ala
65 70 75 80
Arg Lys Asn Val Tyr Arg Gly Ile Arg Gln Arg Pro Trp Gly Lys Trp
85 90 95
Ala Ala Glu Ile Arg Asp Pro His Lys Gly Val Arg Val Trp Leu Gly
100 105 110
Thr Phe Pro Thr Ala Glu Glu Ala Ala Gln Ala Tyr Asp Asp Ala Ala
115 120 125
Ile Arg Ile Arg Gly Asp Lys Ala Lys Leu Asn Phe Pro Ala Thr Thr
130 135 140
Ile Ser Ala Ala Ala Ala Pro Pro Pro Ser Lys Lys Gln Arg Cys Leu
145 150 155 160
Ser Pro Asp Ile Ile Thr Glu Glu Ser Ser Ser Ser Ser His Ser
165 170 175
Thr Thr Gly Ser Thr Gly Glu Ser Gly Gly Asn Asp Glu Leu Asp
180 185 190
Leu Lys Gln Ile Glu Trp Phe Leu Gly Leu Glu Asn Glu Leu Pro Val
195 200 205
Ser Asn Asn Ile Gly Ala Glu Trp Asp Asn Met Asp Asp Leu Trp Met

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210	215	220
Leu Asp Asp Val Val Val	Pro Asn Arg His	Leu Ile Tyr
225	230	235

<210> 10
 <211> 856
 <212> DNA
 <213> Glycine max

<220>
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 <222> (111)...(719)

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 attggtgttt ccaccaaata cagtgagcaa agttagctga aaattaaaac atg gtt 116
 Met Val
 1

tcc gcc acc gtg gat tcc gat ttt gca ttc ttg gaa tct gtt caa caa 164
 Ser Ala Thr Val Asp Ser Asp Phe Ala Phe Leu Glu Ser Val Gln Gln
 5 10 15

tac cta ctt gga cat gat tcc atc aat ctc atg tct gaa acc cac caa 212
 Tyr Leu Leu Gly His Asp Ser Ile Asn Leu Met Ser Glu Thr His Gln
 20 25 30

gct gca tct cat gat cca ttt tca gac cct aat aaa tgt gat ggt gat 260
 Ala Ala Ser His Asp Pro Phe Ser Asp Pro Asn Lys Cys Asp Gly Asp
 35 40 45 50

tca ggg aac att gct ttc cga agt gag gat gca acg gct gtg gta gcg 308
 Ser Gly Asn Ile Ala Phe Arg Ser Glu Asp Ala Thr Ala Val Val Ala
 55 60 65

cgt gat cat gcg cca cca aca tgg aag cat tac aga ggg gtg agg cgt 356
 Arg Asp His Ala Pro Pro Thr Trp Lys His Tyr Arg Gly Val Arg Arg
 70 75 80

aga ccg tgg gga aag ttt gcg gcc gag att agg gat cca aag aag aac 404
 Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Lys Lys Asn
 85 90 95

gga gct agg gtt tgg ctt ggc acg tat gat acc gaa gag aag gcc gct 452
 Gly Ala Arg Val Trp Leu Gly Thr Tyr Asp Thr Glu Glu Lys Ala Ala
 100 105 110

ttg gca tat gac aaa gcc gct ttc aaa atg cga ggc caa aag gcc aag 500
 Leu Ala Tyr Asp Lys Ala Ala Phe Lys Met Arg Gly Gln Lys Ala Lys
 115 120 125 130

ctg aat ttt cct cat ctt att gat tcc gac aat tcc gat gaa ttg tcg 548
 Leu Asn Phe Pro His Leu Ile Asp Ser Asp Asn Ser Asp Glu Leu Ser
 135 140 145

gag cca gta atg atg aca act tcc aag cga agt ttg tta gaa att tca 596
 Glu Pro Val Met Met Thr Thr Ser Lys Arg Ser Leu Leu Glu Ile Ser

150	155	160	
tca ccg tcg tcc tcg tgt tca gat gat agc tca gaa tca caa ggg aca			644
Ser Pro Ser Ser Ser Cys Ser Asp Asp Ser Ser Glu Ser Gln Gly Thr			
165	170	175	
aag agg agg aag agc ctg gct gaa cta ctg aat aaa tta gcc aag aat			692
Lys Arg Arg Lys Ser Leu Ala Glu Leu Leu Asn Lys Leu Ala Lys Asn			
180	185	190	
aga agc caa gtc aag gtg gaa tgt tga agtggctaga ggaatatgca			739
Arg Ser Gln Val Lys Val Glu Cys *			
195	200		
tgttgtacaa tttgatcaat cattaatatg agacttcaac gattgtaatg taatctggtg			799
ttcatagaat taatgcaatt ttgttcacca aaaaaaaaaa aaaaaaaaaa aaaaaaa			856

<210> 11
 <211> 202
 <212> PRT
 <213> Glycine max

<400> 11
 Met Val Ser Ala Thr Val Asp Ser Asp Phe Ala Phe Leu Glu Ser Val
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 Gln Gln Tyr Leu Leu Gly His Asp Ser Ile Asn Leu Met Ser Glu Thr
 20 25 30
 His Gln Ala Ala Ser His Asp Pro Phe Ser Asp Pro Asn Lys Cys Asp
 35 40 45
 Gly Asp Ser Gly Asn Ile Ala Phe Arg Ser Glu Asp Ala Thr Ala Val
 50 55 60
 Val Ala Arg Asp His Ala Pro Pro Thr Trp Lys His Tyr Arg Gly Val
 65 70 75 80
 Arg Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Lys
 85 90 95
 Lys Asn Gly Ala Arg Val Trp Leu Gly Thr Tyr Asp Thr Glu Glu Lys
 100 105 110
 Ala Ala Leu Ala Tyr Asp Lys Ala Ala Phe Lys Met Arg Gly Gln Lys
 115 120 125
 Ala Lys Leu Asn Phe Pro His Leu Ile Asp Ser Asp Asn Ser Asp Glu
 130 135 140
 Leu Ser Glu Pro Val Met Met Thr Thr Ser Lys Arg Ser Leu Leu Glu
 145 150 155 160
 Ile Ser Ser Pro Ser Ser Ser Cys Ser Asp Asp Ser Ser Glu Ser Gln
 165 170 175
 Gly Thr Lys Arg Arg Lys Ser Leu Ala Glu Leu Leu Asn Lys Leu Ala
 180 185 190
 Lys Asn Arg Ser Gln Val Lys Val Glu Cys
 195 200

<210> 12
 <211> 854
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS

<222> (115)...(723)

<400> 12

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gaattcggca cgagccacca aatacagtga gcaaagttag ctgaaaatta aaac atg 117
                                         Met
                                         1

gtt tcc gcc acc gtg gat tcc gat ttt gca ttc ttg gaa tct gtt caa 165
Val Ser Ala Thr Val Asp Ser Asp Phe Ala Phe Leu Glu Ser Val Gln
                    5                      10                      15

caa tac cta ctt gga cat gat tcc atc aat ctc atg tct gaa acc cac 213
Gln Tyr Leu Leu Gly His Asp Ser Ile Asn Leu Met Ser Glu Thr His
                    20                      25                      30

caa gct gca tct cat gat cca ttt tca gac cct aat aaa tgt gat ggt 261
Gln Ala Ala Ser His Asp Pro Phe Ser Asp Pro Asn Lys Cys Asp Gly
                    35                      40                      45

gat tca ggg aac att gct ttc cga agt gag gat gca acg gct gtg gtg 309
Asp Ser Gly Asn Ile Ala Phe Arg Ser Glu Asp Ala Thr Ala Val Val
                    50                      55                      60                      65

gct cgt gat cat gcg cca caa aca tgg aag cat tac aga ggg gtg aga 357
Ala Arg Asp His Ala Pro Gln Thr Trp Lys His Tyr Arg Gly Val Arg
                    70                      75                      80

cgt aga ccg tgg gga aag ttt gcg gcc gag att agg gat cca aag aag 405
Arg Arg Pro Trp Gly Lys Phe Ala Ala Glu Ile Arg Asp Pro Lys Lys
                    85                      90                      95

aac gga gct agg gtt tgg ctt ggc acg tat gat acc gaa gag aag gcg 453
Asn Gly Ala Arg Val Trp Leu Gly Thr Tyr Asp Thr Glu Glu Lys Ala
                    100                      105                      110

gct ttg gca tat gac aaa gcc gct ttc aaa atg cga ggc caa aag gcc 501
Ala Leu Ala Tyr Asp Lys Ala Ala Phe Lys Met Arg Gly Gln Lys Ala
                    115                      120                      125

aag ctg aat ttt cct cat ctt att gat tcc gac aat tcc gat gaa ttg 549
Lys Leu Asn Phe Pro His Leu Ile Asp Ser Asp Asn Ser Asp Glu Leu
                    130                      135                      140                      145

tcg gag cca gta atg atg aca act tcc aag cga agt ttg tta gaa att 597
Ser Glu Pro Val Met Met Thr Thr Ser Lys Arg Ser Leu Leu Glu Ile
                    150                      155                      160

tca tca ccg tcg tcc tcg tat tca gat gat agc tca gaa tca caa ggg 645
Ser Ser Pro Ser Ser Ser Tyr Ser Asp Asp Ser Ser Glu Ser Gln Gly
                    165                      170                      175

aca aag agg agg aag agc ctt gct gaa cta ctg aat aaa tta gcc aag 693
Thr Lys Arg Arg Lys Ser Leu Ala Glu Leu Leu Asn Lys Leu Ala Lys
                    180                      185                      190

aat aga agc caa gtc aag gtg gaa tgt tga agtggctaga tgaatatgca 743
Asn Arg Ser Gln Val Lys Val Glu Cys *

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195

200

tggtgtacaa tttgatcaat cattaatatg agacttcaac gattgtaatg taatctgggtg 803
 ttcatagaat taatgcaatt ttgttcacca taaaaaaaaa aaaaaaaaaa a 854

<210> 13

<211> 202

<212> PRT

<213> Glycine max

<400> 13

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Gln	Gln	Tyr	Leu	Gly	His	Asp	Ser	Ile	Asn	Leu	Met	Ser	Glu	Thr	
			20				25					30			
His	Gln	Ala	Ala	Ser	His	Asp	Pro	Phe	Ser	Asp	Pro	Asn	Lys	Cys	Asp
		35				40						45			
Gly	Asp	Ser	Gly	Asn	Ile	Ala	Phe	Arg	Ser	Glu	Asp	Ala	Thr	Ala	Val
	50					55					60				
Val	Ala	Arg	Asp	His	Ala	Pro	Gln	Thr	Trp	Lys	His	Tyr	Arg	Gly	Val
65					70					75					80
Arg	Arg	Arg	Pro	Trp	Gly	Lys	Phe	Ala	Ala	Glu	Ile	Arg	Asp	Pro	Lys
				85				90						95	
Lys	Asn	Gly	Ala	Arg	Val	Trp	Leu	Gly	Thr	Tyr	Asp	Thr	Glu	Glu	Lys
			100					105					110		
Ala	Ala	Leu	Ala	Tyr	Asp	Lys	Ala	Ala	Phe	Lys	Met	Arg	Gly	Gln	Lys
		115					120					125			
Ala	Lys	Leu	Asn	Phe	Pro	His	Leu	Ile	Asp	Ser	Asp	Asn	Ser	Asp	Glu
	130					135					140				
Leu	Ser	Glu	Pro	Val	Met	Met	Thr	Thr	Ser	Lys	Arg	Ser	Leu	Leu	Glu
145					150					155					160
Ile	Ser	Ser	Pro	Ser	Ser	Ser	Tyr	Ser	Asp	Asp	Ser	Ser	Glu	Ser	Gln
				165					170					175	
Gly	Thr	Lys	Arg	Arg	Lys	Ser	Leu	Ala	Glu	Leu	Leu	Asn	Lys	Leu	Ala
			180					185					190		
Lys	Asn	Arg	Ser	Gln	Val	Lys	Val	Glu	Cys						
		195					200								

<210> 14

<211> 858

<212> DNA

<213> Glycine max

<220>

<221> CDS

<222> (7)...(648)

<400> 14

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	Met	Lys	Thr	Lys	Leu	Leu	Ala	Phe	Leu	Leu	Phe	Phe	Ala	Leu	
	1				5						10				
act	aca	aaa	cca	cta	cta	ctt	gga	gca	gct	gga	gct	gct	cca	gag	cca
Thr	Thr	Lys	Pro	Leu	Leu	Leu	Gly	Ala	Ala	Gly	Ala	Ala	Pro	Glu	Pro
	15				20					25				30	
gtg	att	gat	aca	tca	ggc	aag	aag	ctg	aga	gct	gat	gca	aat	tac	cat
															144

Val	Ile	Asp	Thr	Ser	Gly	Lys	Lys	Leu	Arg	Ala	Asp	Ala	Asn	Tyr	His	
				35					40					45		
atc	atc	cct	gca	gtg	ccc	ttc	acc	ata	tgt	ggc	ttt	gtt	agc	tgt	ttc	192
Ile	Ile	Pro	Ala	Val	Pro	Phe	Thr	Ile	Cys	Gly	Phe	Val	Ser	Cys	Phe	
			50					55					60			
act	ggt	gga	ggc	ctt	tca	cta	gac	agc	ata	gat	gaa	tct	tgc	cct	ctt	240
Thr	Gly	Gly	Gly	Leu	Ser	Leu	Asp	Ser	Ile	Asp	Glu	Ser	Cys	Pro	Leu	
		65					70					75				
gat	gta	ata	att	gag	aaa	gcc	aat	gaa	ggc	cta	cca	ctg	aga	ttc	tca	288
Asp	Val	Ile	Ile	Glu	Lys	Ala	Asn	Glu	Gly	Leu	Pro	Leu	Arg	Phe	Ser	
	80					85					90					
cca	gtt	aac	acc	aaa	aaa	ggg	gtt	att	cgt	gtc	tcc	acc	gat	ttg	aac	336
Pro	Val	Asn	Thr	Lys	Lys	Gly	Val	Ile	Arg	Val	Ser	Thr	Asp	Leu	Asn	
	95				100					105					110	
att	ttt	ttc	tct	gat	tct	gat	gaa	agg	tgt	cca	cac	cat	tcc	act	gtg	384
Ile	Phe	Phe	Ser	Asp	Ser	Asp	Glu	Arg	Cys	Pro	His	His	Ser	Thr	Val	
				115					120					125		
tgg	atg	ctt	gat	caa	ttt	gat	gcc	tct	att	gga	cag	aca	tat	gtg	acc	432
Trp	Met	Leu	Asp	Gln	Phe	Asp	Ala	Ser	Ile	Gly	Gln	Thr	Tyr	Val	Thr	
			130					135					140			
act	ggt	ggt	gtt	gtt	gga	aac	ccg	ggt	gag	cac	aca	att	ctg	aat	tgg	480
Thr	Gly	Gly	Val	Val	Gly	Asn	Pro	Gly	Glu	His	Thr	Ile	Leu	Asn	Trp	
		145					150					155				
ttc	aag	att	cag	aag	tat	gag	gat	gct	tat	aag	ctg	gtc	tat	tgc	cct	528
Phe	Lys	Ile	Gln	Lys	Tyr	Glu	Asp	Ala	Tyr	Lys	Leu	Val	Tyr	Cys	Pro	
	160					165					170					
agg	gtg	tgc	ccc	tct	tgc	cac	cat	ctg	tgc	aag	gat	att	gga	atg	ttt	576
Arg	Val	Cys	Pro	Ser	Cys	His	His	Leu	Cys	Lys	Asp	Ile	Gly	Met	Phe	
	175				180					185					190	
gtg	gat	gcc	aat	agg	aga	atg	cat	ctg	gct	ctc	agt	gat	gat	ccc	ttc	624
Val	Asp	Ala	Asn	Arg	Arg	Met	His	Leu	Ala	Leu	Ser	Asp	Asp	Pro	Phe	
				195				200						205		
aaa	att	aag	ttc	aaa	gaa	gcc	tga	gatcaaagct	ctttcaaagt	atggcaaaaat						678
Lys	Ile	Lys	Phe	Lys	Glu	Ala	*									
			210													
taaatgacaa	tccatgaata	cgtgtgttta	taatgatcga	tccttgaaat	tatatatttctt											738
tgtgaagaat	tagtaaatga	ataaaaaaaaaat	taagagtgtgta	tgttttttgtc	ctgctgtttac											798
aactttaatt	tcactatttaa	ataataaata	caattttttaa	taaaaaaaaaa	aaaaaaaaaaaa											858

<210> 15

<211> 213

<212> PRT

<213> Glycine max

<400> 15

Met	Lys	Thr	Lys	Leu	Leu	Ala	Phe	Leu	Leu	Phe	Phe	Ala	Leu	Thr	Thr
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Lys	Pro	Leu	Leu	Leu	Gly	Ala	Ala	Gly	Ala	Ala	Pro	Glu	Pro	Val	Ile
			20					25					30		
Asp	Thr	Ser	Gly	Lys	Lys	Leu	Arg	Ala	Asp	Ala	Asn	Tyr	His	Ile	Ile
		35					40				45				
Pro	Ala	Val	Pro	Phe	Thr	Ile	Cys	Gly	Phe	Val	Ser	Cys	Phe	Thr	Gly
		50				55					60				
Gly	Gly	Leu	Ser	Leu	Asp	Ser	Ile	Asp	Glu	Ser	Cys	Pro	Leu	Asp	Val
65					70					75				80	
Ile	Ile	Glu	Lys	Ala	Asn	Glu	Gly	Leu	Pro	Leu	Arg	Phe	Ser	Pro	Val
				85					90					95	
Asn	Thr	Lys	Lys	Gly	Val	Ile	Arg	Val	Ser	Thr	Asp	Leu	Asn	Ile	Phe
			100					105					110		
Phe	Ser	Asp	Ser	Asp	Glu	Arg	Cys	Pro	His	His	Ser	Thr	Val	Trp	Met
		115					120					125			
Leu	Asp	Gln	Phe	Asp	Ala	Ser	Ile	Gly	Gln	Thr	Tyr	Val	Thr	Thr	Gly
		130				135					140				
Gly	Val	Val	Gly	Asn	Pro	Gly	Glu	His	Thr	Ile	Leu	Asn	Trp	Phe	Lys
145					150					155					160
Ile	Gln	Lys	Tyr	Glu	Asp	Ala	Tyr	Lys	Leu	Val	Tyr	Cys	Pro	Arg	Val
				165					170					175	
Cys	Pro	Ser	Cys	His	His	Leu	Cys	Lys	Asp	Ile	Gly	Met	Phe	Val	Asp
			180					185				190			
Ala	Asn	Arg	Arg	Met	His	Leu	Ala	Leu	Ser	Asp	Asp	Pro	Phe	Lys	Ile
		195					200					205			
Lys	Phe	Lys	Glu	Ala											
			210												

<210> 16

<211> 846

<212> DNA

<213> Glycine max

<220>

<221> CDS

<222> (33)...(662)

<400> 16

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				1				5								
gca	ttt	gcc	ctt	gtc	tta	gcc	ttg	agt	tca	caa	cca	ctg	cta	gga	gga	101
Ala	Phe	Ala	Leu	Val	Leu	Ala	Leu	Ser	Ser	Gln	Pro	Leu	Leu	Gly	Gly	
		10					15					20				
gct	gaa	gcc	tca	ccc	gag	caa	gtg	gtt	gac	aca	tta	ggc	aag	aag	ctc	149
Ala	Glu	Ala	Ser	Pro	Glu	Gln	Val	Val	Asp	Thr	Leu	Gly	Lys	Lys	Leu	
		25				30					35					
cga	gtt	gga	acc	aat	tac	tat	att	gtc	cca	tct	ctt	ccc	tac	acc	aaa	197
Arg	Val	Gly	Thr	Asn	Tyr	Tyr	Ile	Val	Pro	Ser	Leu	Pro	Tyr	Thr	Lys	
		40			45				50						55	
att	aga	acc	act	aga	ggc	ctt	ggc	cta	gcc	agt	gtt	gga	aaa	cct	tat	245
Ile	Arg	Thr	Thr	Arg	Gly	Leu	Gly	Leu	Ala	Ser	Val	Gly	Lys	Pro	Tyr	

60										65					70					
tgt	cct	ctt	gat	gtt	gtg	gtt	gtg	aat	gga	tac	cat	ggc	ttg	cca	gtg	293				
Cys	Pro	Leu	Asp	Val	Val	Val	Val	Asn	Gly	Tyr	His	Gly	Leu	Pro	Val					
			75					80					85							
aca	ttc	tca	cca	gtt	aat	cct	aag	aaa	ggg	gtc	att	cgt	gtc	tca	act	341				
Thr	Phe	Ser	Pro	Val	Asn	Pro	Lys	Lys	Gly	Val	Ile	Arg	Val	Ser	Thr					
		90					95					100								
gat	ttg	aac	atc	aag	ttc	tct	gct	cgc	act	agt	tgt	ccc	cgc	caa	tat	389				
Asp	Leu	Asn	Ile	Lys	Phe	Ser	Ala	Arg	Thr	Ser	Cys	Pro	Arg	Gln	Tyr					
	105					110					115									
tcc	acg	gtt	tgg	aaa	ctt	gat	gat	ttt	gat	ttc	tca	aag	aga	caa	tgg	437				
Ser	Thr	Val	Trp	Lys	Leu	Asp	Asp	Phe	Asp	Phe	Ser	Lys	Arg	Gln	Trp					
120					125					130					135					
ttt	gtg	acc	act	ggt	ggt	gtt	gtg	gga	aac	cct	agc	ttg	gaa	acc	atc	485				
Phe	Val	Thr	Thr	Gly	Gly	Val	Val	Gly	Asn	Pro	Ser	Leu	Glu	Thr	Ile					
				140					145					150						
cac	aac	tgg	ttc	aag	att	gag	aag	tac	gat	ggt	gct	tac	aaa	ttg	gtc	533				
His	Asn	Trp	Phe	Lys	Ile	Glu	Lys	Tyr	Asp	Gly	Ala	Tyr	Lys	Leu	Val					
		155						160					165							
tat	tgt	ccc	agc	gtg	gtg	aaa	tgt	cca	aag	cat	ttg	tgc	aag	aat	gtt	581				
Tyr	Cys	Pro	Ser	Val	Val	Lys	Cys	Pro	Lys	His	Leu	Cys	Lys	Asn	Val					
		170					175					180								
ggg	ttg	ttt	gtg	gat	gag	aaa	ggg	aac	aag	cgt	ctt	gct	ctc	act	gat	629				
Gly	Leu	Phe	Val	Asp	Glu	Lys	Gly	Asn	Lys	Arg	Leu	Ala	Leu	Thr	Asp					
	185					190					195									
gtt	ccc	ctc	aaa	gtt	caa	ttc	caa	caa	gcc	taa	acaagcttaa	tgctcctcta				682				
Val	Pro	Leu	Lys	Val	Gln	Phe	Gln	Gln	Ala	*										
200					205															
agtcta	acat	taatgc	ataa	aaactat	ata	tgaata	agtg	tatttc	ccttt	ctaata	acga					742				
tgcatg	ttct	ttcaat	gttt	atcagg	atcc	tcatgt	aaagg	ttttc	ccttg	taaatg	caaa					802				
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<210> 17

<211> 209

<212> PRT

<213> Glycine max

<400> 17

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		20						25					30		
Asp	Thr	Leu	Gly	Lys	Lys	Leu	Arg	Val	Gly	Thr	Asn	Tyr	Tyr	Ile	Val
		35					40					45			
Pro	Ser	Leu	Pro	Tyr	Thr	Lys	Ile	Arg	Thr	Thr	Arg	Gly	Leu	Gly	Leu
	50					55					60				
Ala	Ser	Val	Gly	Lys	Pro	Tyr	Cys	Pro	Leu	Asp	Val	Val	Val	Val	Asn
65					70					75					80

Gly	Tyr	His	Gly	Leu	Pro	Val	Thr	Phe	Ser	Pro	Val	Asn	Pro	Lys	Lys
			85						90					95	
Gly	Val	Ile	Arg	Val	Ser	Thr	Asp	Leu	Asn	Ile	Lys	Phe	Ser	Ala	Arg
			100					105					110		
Thr	Ser	Cys	Pro	Arg	Gln	Tyr	Ser	Thr	Val	Trp	Lys	Leu	Asp	Asp	Phe
		115					120					125			
Asp	Phe	Ser	Lys	Arg	Gln	Trp	Phe	Val	Thr	Thr	Gly	Gly	Val	Val	Gly
	130					135					140				
Asn	Pro	Ser	Leu	Glu	Thr	Ile	His	Asn	Trp	Phe	Lys	Ile	Glu	Lys	Tyr
145					150					155					160
Asp	Gly	Ala	Tyr	Lys	Leu	Val	Tyr	Cys	Pro	Ser	Val	Val	Lys	Cys	Pro
			165					170						175	
Lys	His	Leu	Cys	Lys	Asn	Val	Gly	Leu	Phe	Val	Asp	Glu	Lys	Gly	Asn
		180						185					190		
Lys	Arg	Leu	Ala	Leu	Thr	Asp	Val	Pro	Leu	Lys	Val	Gln	Phe	Gln	Gln
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Ala

<210> 18
 <211> 1410
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
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 Met Ala Ser Met Asn Asn Gln Lys
 1 5

gaa att gag ctc ttt gag ggc caa tct ctt ctg tac atg cag cta tat 102
 Glu Ile Glu Leu Phe Glu Gly Gln Ser Leu Leu Tyr Met Gln Leu Tyr
 10 15 20

ggg cac cta aga cct atg tgt ctt aag tgg gct gtt caa cta ggt att 150
 Gly His Leu Arg Pro Met Cys Leu Lys Trp Ala Val Gln Leu Gly Ile
 25 30 35 40

cca gac ata ata cag aac cat gcc aaa ccc att tct ctt tct gac ttg 198
 Pro Asp Ile Ile Gln Asn His Ala Lys Pro Ile Ser Leu Ser Asp Leu
 45 50 55

gtc tct act ctt caa att cca cca gct aac gct gct ttt gtg cag cg 246
 Val Ser Thr Leu Gln Ile Pro Pro Ala Asn Ala Ala Phe Val Gln Arg
 60 65 70

ttc atg cgc ttc ttg gca cac aat gga atc ttt gag atc cat gag agc 294
 Phe Met Arg Phe Leu Ala His Asn Gly Ile Phe Glu Ile His Glu Ser
 75 80 85

caa gaa gat cat gaa cta aca tat gct cta acc cct gca tca aag ctt 342
 Gln Glu Asp His Glu Leu Thr Tyr Ala Leu Thr Pro Ala Ser Lys Leu
 90 95 100

ctt gtc aat agt agt gat cat tgt cta tct cca atg gtt cta gcg ttt	390
Leu Val Asn Ser Ser Asp His Cys Leu Ser Pro Met Val Leu Ala Phe	
105 110 115 120	
acc gat cca ctt cgg aac gtt aaa tac cat cac ttg ggg gaa tgg att	438
Thr Asp Pro Leu Arg Asn Val Lys Tyr His His Leu Gly Glu Trp Ile	
125 130 135	
cgt ggg gag gac ccc tca gta ttt gag aca gcc cac gga aca agc gct	486
Arg Gly Glu Asp Pro Ser Val Phe Glu Thr Ala His Gly Thr Ser Ala	
140 145 150	
tgg gga ctt ctt gag aaa aat cct gaa tat ttt agt ctc ttc aat gag	534
Trp Gly Leu Leu Glu Lys Asn Pro Glu Tyr Phe Ser Leu Phe Asn Glu	
155 160 165	
gct atg gca agt gat tcc cga ata gta gac ttg gca ctc aaa aat tgc	582
Ala Met Ala Ser Asp Ser Arg Ile Val Asp Leu Ala Leu Lys Asn Cys	
170 175 180	
act tca gtt ttt gag ggg cta gat tcc atg gtg gat gtt ggt ggt gga	630
Thr Ser Val Phe Glu Gly Leu Asp Ser Met Val Asp Val Gly Gly Gly	
185 190 195 200	
act gga acc acg gcc aga att atc tgt gac gca ttt cct aag ttg aaa	678
Thr Gly Thr Thr Ala Arg Ile Ile Cys Asp Ala Phe Pro Lys Leu Lys	
205 210 215	
tgt gtt gtg ctt gac ctt cct cat gtt gta gag aac ttg aca ggg acc	726
Cys Val Val Leu Asp Leu Pro His Val Val Glu Asn Leu Thr Gly Thr	
220 225 230	
aat aat ttg agt ttt gtt ggt ggt gac atg ttc aac tct atc cct caa	774
Asn Asn Leu Ser Phe Val Gly Gly Asp Met Phe Asn Ser Ile Pro Gln	
235 240 245	
gct gat gca gtg cta cta aag tgg gtt tta cat aat tgg acc gac gaa	822
Ala Asp Ala Val Leu Leu Lys Trp Val Leu His Asn Trp Thr Asp Glu	
250 255 260	
aat tgc ata aag atc ctg caa aag tgt aga gat tct att tca agc aaa	870
Asn Cys Ile Lys Ile Leu Gln Lys Cys Arg Asp Ser Ile Ser Ser Lys	
265 270 275 280	
ggc aac agt gga aaa gtg att atc ata gat gcc gta ata aat gag aag	918
Gly Asn Ser Gly Lys Val Ile Ile Ile Asp Ala Val Ile Asn Glu Lys	
285 290 295	
cta gat gac ccg gat atg aca caa aca aag ctt agt ttg gac att att	966
Leu Asp Asp Pro Asp Met Thr Gln Thr Lys Leu Ser Leu Asp Ile Ile	
300 305 310	
atg ttg acg atg aat gga aga gag aga acg gaa aaa gaa tgg aaa caa	1014
Met Leu Thr Met Asn Gly Arg Glu Arg Thr Glu Lys Glu Trp Lys Gln	
315 320 325	
ctc ttc atc gaa gca gga ttc aaa cac tac aaa ata ttt ccc atc ttt	1062
Leu Phe Ile Glu Ala Gly Phe Lys His Tyr Lys Ile Phe Pro Ile Phe	

330

335

340

ggg ttt aga tct ctg att gag gtc tat cct tga acatttttat gatgtgtatg 1115
 Gly Phe Arg Ser Leu Ile Glu Val Tyr Pro *
 345 350

tcacacttaa cgtttatatt tatgaacatc ctcagacatc gttgtaattg tatttagtgg 1175
 tttgcgtgtt gtttgctgaa taaagctatg atgacatagc attatcaact tctgggtggaa 1235
 ttacattatg ttctcccccg ctatgttgtt aaatgttctg tgtacggatt tctcattcct 1295
 atttggccaa aataaattga ataaacatgt aatggatgca atcaatatac aatgttttgg 1355
 tatggcttta cgtcttttaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1410

<210> 19

<211> 354

<212> PRT

<213> Glycine max

<400> 19

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			20					25					30		
Lys	Trp	Ala	Val	Gln	Leu	Gly	Ile	Pro	Asp	Ile	Ile	Gln	Asn	His	Ala
			35				40					45			
Lys	Pro	Ile	Ser	Leu	Ser	Asp	Leu	Val	Ser	Thr	Leu	Gln	Ile	Pro	Pro
			50			55					60				
Ala	Asn	Ala	Ala	Phe	Val	Gln	Arg	Phe	Met	Arg	Phe	Leu	Ala	His	Asn
65				70				75						80	
Gly	Ile	Phe	Glu	Ile	His	Glu	Ser	Gln	Glu	Asp	His	Glu	Leu	Thr	Tyr
			85					90						95	
Ala	Leu	Thr	Pro	Ala	Ser	Lys	Leu	Leu	Val	Asn	Ser	Ser	Asp	His	Cys
			100					105					110		
Leu	Ser	Pro	Met	Val	Leu	Ala	Phe	Thr	Asp	Pro	Leu	Arg	Asn	Val	Lys
			115				120					125			
Tyr	His	His	Leu	Gly	Glu	Trp	Ile	Arg	Gly	Glu	Asp	Pro	Ser	Val	Phe
			130			135					140				
Glu	Thr	Ala	His	Gly	Thr	Ser	Ala	Trp	Gly	Leu	Leu	Glu	Lys	Asn	Pro
145				150						155				160	
Glu	Tyr	Phe	Ser	Leu	Phe	Asn	Glu	Ala	Met	Ala	Ser	Asp	Ser	Arg	Ile
			165					170						175	
Val	Asp	Leu	Ala	Leu	Lys	Asn	Cys	Thr	Ser	Val	Phe	Glu	Gly	Leu	Asp
			180					185					190		
Ser	Met	Val	Asp	Val	Gly	Gly	Gly	Thr	Gly	Thr	Thr	Ala	Arg	Ile	Ile
			195				200					205			
Cys	Asp	Ala	Phe	Pro	Lys	Leu	Lys	Cys	Val	Val	Leu	Asp	Leu	Pro	His
			210			215					220				
Val	Val	Glu	Asn	Leu	Thr	Gly	Thr	Asn	Asn	Leu	Ser	Phe	Val	Gly	Gly
225				230						235				240	
Asp	Met	Phe	Asn	Ser	Ile	Pro	Gln	Ala	Asp	Ala	Val	Leu	Leu	Lys	Trp
			245					250						255	
Val	Leu	His	Asn	Trp	Thr	Asp	Glu	Asn	Cys	Ile	Lys	Ile	Leu	Gln	Lys
			260				265						270		
Cys	Arg	Asp	Ser	Ile	Ser	Ser	Lys	Gly	Asn	Ser	Gly	Lys	Val	Ile	Ile
			275				280					285			
Ile	Asp	Ala	Val	Ile	Asn	Glu	Lys	Leu	Asp	Asp	Pro	Asp	Met	Thr	Gln
			290			295					300				
Thr	Lys	Leu	Ser	Leu	Asp	Ile	Ile	Met	Leu	Thr	Met	Asn	Gly	Arg	Glu
305				310						315				320	

Arg	Thr	Glu	Lys	Glu	Trp	Lys	Gln	Leu	Phe	Ile	Glu	Ala	Gly	Phe	Lys
				325					330					335	
His	Tyr	Lys	Ile	Phe	Pro	Ile	Phe	Gly	Phe	Arg	Ser	Leu	Ile	Glu	Val
			340					345					350		
Tyr	Pro														

<210> 20
 <211> 1630
 <212> DNA
 <213> Glycine max

<220>
 <221> CDS
 <222> (93)...(1403)

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cctcgattag tgtatgcaaa tttcttttagg ac atg tgg cct aca tta gtg gct															113	
									Met	Trp	Pro	Thr	Leu	Val	Ala	
									1				5			
aat	aag	ata	ttc	aag	aag	aga	ctt	gga	agc	agc	aat	ttt	ata	gcg	gat	161
Asn	Lys	Ile	Phe	Lys	Lys	Arg	Leu	Gly	Ser	Ser	Asn	Phe	Ile	Ala	Asp	
			10					15					20			
tat	cct	agt	tat	aaa	gaa	ccc	ttg	ctg	ggt	att	gta	gac	att	gat	cag	209
Tyr	Pro	Ser	Tyr	Lys	Glu	Pro	Leu	Leu	Gly	Ile	Val	Asp	Ile	Asp	Gln	
			25				30					35				
aac	tca	aaa	acc	att	ctt	aat	gat	cac	aag	gac	tca	cac	aaa	tac	aag	257
Asn	Ser	Lys	Thr	Ile	Leu	Asn	Asp	His	Lys	Asp	Ser	His	Lys	Tyr	Lys	
			40			45				50					55	
gta	ttt	gtt	agt	aca	tgg	aac	gta	ggt	ggg	att	gca	ccg	gat	gaa	gat	305
Val	Phe	Val	Ser	Thr	Trp	Asn	Val	Gly	Gly	Ile	Ala	Pro	Asp	Glu	Asp	
				60					65					70		
ttg	aat	ata	gat	gat	ttg	ttg	gag	aca	tgc	aac	aac	tct	tgt	gac	atc	353
Leu	Asn	Ile	Asp	Asp	Leu	Leu	Glu	Thr	Cys	Asn	Asn	Ser	Cys	Asp	Ile	
			75					80					85			
tat	ata	cta	ggg	ttt	caa	gaa	ata	gtg	cct	cta	aaa	gca	tca	aat	gta	401
Tyr	Ile	Leu	Gly	Phe	Gln	Glu	Ile	Val	Pro	Leu	Lys	Ala	Ser	Asn	Val	
			90				95						100			
ttg	ggg	tcc	gaa	aac	aat	gag	att	tct	atg	aaa	tgg	aat	tcc	ata	atc	449
Leu	Gly	Ser	Glu	Asn	Asn	Glu	Ile	Ser	Met	Lys	Trp	Asn	Ser	Ile	Ile	
			105			110					115					
agg	gaa	gcc	ttg	aac	aag	aaa	ata	aca	cat	caa	agg	gac	aaa	gat	gct	497
Arg	Glu	Ala	Leu	Asn	Lys	Lys	Ile	Thr	His	Gln	Arg	Asp	Lys	Asp	Ala	
			120			125				130					135	
aaa	aaa	cag	gag	cta	aag	aat	aat	ttt	ccc	aat	aag	aaa	gaa	aat	cca	545
Lys	Lys	Gln	Glu	Leu	Lys	Asn	Asn	Phe	Pro	Asn	Lys	Lys	Glu	Asn	Pro	
				140					145					150		

gct aag tgc tgt gat gcc cca cat gat ttc caa tgt atc att agc aag	593
Ala Lys Cys Cys Asp Ala Pro His Asp Phe Gln Cys Ile Ile Ser Lys	
155 160 165	
caa atg gtt gga tta ttc ata tct gtg tgg att aga aga gat ctt tgt	641
Gln Met Val Gly Leu Phe Ile Ser Val Trp Ile Arg Arg Asp Leu Cys	
170 175 180	
cca ttc att cgg cat cca agc gtg tca tgt gta ggt tgt ggg ata atg	689
Pro Phe Ile Arg His Pro Ser Val Ser Cys Val Gly Cys Gly Ile Met	
185 190 195	
ggc tgc tta gga aac aag ggt tct ata tca gtg aga ttt cag tta cat	737
Gly Cys Leu Gly Asn Lys Gly Ser Ile Ser Val Arg Phe Gln Leu His	
200 205 210 215	
gaa acc agc ttc tgc ttt gtg tgc agc cat cta gct tca ggg ggc aga	785
Glu Thr Ser Phe Cys Phe Val Cys Ser His Leu Ala Ser Gly Gly Arg	
220 225 230	
gaa ggg gat gag aag cac agg aac tct aat gtt gct gaa att ttt tct	833
Glu Gly Asp Glu Lys His Arg Asn Ser Asn Val Ala Glu Ile Phe Ser	
235 240 245	
cgg aca agt ttt cct aga ggc cct ttg ctt gat ttg cct aga acc att	881
Arg Thr Ser Phe Pro Arg Gly Pro Leu Leu Asp Leu Pro Arg Thr Ile	
250 255 260	
ctt gat cat gat cat gta ata ttg ctt gga gat cta aat tac aga att	929
Leu Asp His Asp His Val Ile Leu Leu Gly Asp Leu Asn Tyr Arg Ile	
265 270 275	
tct cta cca gaa gaa acc aca cgc ttg ctt gtt gaa aaa aga gac tgg	977
Ser Leu Pro Glu Glu Thr Thr Arg Leu Leu Val Glu Lys Arg Asp Trp	
280 285 290 295	
gat tct tta tta gca aat gat cag cta ata atg gag cta atg agt gga	1025
Asp Ser Leu Leu Ala Asn Asp Gln Leu Ile Met Glu Leu Met Ser Gly	
300 305 310	
aac atg tta aga gga tgg cac gaa gga gca att aaa ttt gca cct acc	1073
Asn Met Leu Arg Gly Trp His Glu Gly Ala Ile Lys Phe Ala Pro Thr	
315 320 325	
tac aaa tat tgt cca aat tca gac att tac tat gga tgc tgc tat cat	1121
Tyr Lys Tyr Cys Pro Asn Ser Asp Ile Tyr Tyr Gly Cys Cys Tyr His	
330 335 340	
ggc aaa aag gca gaa aag aga aga gca cca gca tgg tgt gat cga ata	1169
Gly Lys Lys Ala Glu Lys Arg Arg Ala Pro Ala Trp Cys Asp Arg Ile	
345 350 355	
gta tgg tgc ggt gag ggt cta aag caa ctt cag tac act aga att gaa	1217
Val Trp Cys Gly Glu Gly Leu Lys Gln Leu Gln Tyr Thr Arg Ile Glu	
360 365 370 375	
tca aaa cta tca gat cat agg cct gtt aag gca atg ttt ata gca gaa	1265

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Ser Lys Leu Ser Asp His Arg Pro Val Lys Ala Met Phe Ile Ala Glu
      380      385      390

gtc agg gtt tta cca gag ctg atg aaa aac ttg caa agc ttg ttc cta 1313
Val Arg Val Leu Pro Glu Leu Met Lys Asn Leu Gln Ser Leu Phe Leu
      395      400      405

tca gaa aga tac gag caa att aaa act ccc ttt gaa gtt tcc acc act 1361
Ser Glu Arg Tyr Glu Gln Ile Lys Thr Pro Phe Glu Val Ser Thr Thr
      410      415      420

gaa gat ttt gta aat aga aaa cga tca agc ttc cgg ttg tga 1403
Glu Asp Phe Val Asn Arg Lys Arg Ser Ser Phe Arg Leu *
      425      430      435

attttttgtg tgattcaagc taggctttaa attgtgattg tgattaatgt tgcaatttta 1463
tcacaatctt ttgtggagaa aaatttgcat aaaaatgtga ttgatgtgac cgttattaca 1523
atcagggact tcaacaaccg tgacattgtc atcactgttg tggttgcaca tggttttttt 1583
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<210> 21
 <211> 436
 <212> PRT
 <213> Glycine max

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      20      25      30
Gly Ile Val Asp Ile Asp Gln Asn Ser Lys Thr Ile Leu Asn Asp His
      35      40      45
Lys Asp Ser His Lys Tyr Lys Val Phe Val Ser Thr Trp Asn Val Gly
      50      55      60
Gly Ile Ala Pro Asp Glu Asp Leu Asn Ile Asp Asp Leu Leu Glu Thr
      65      70      75      80
Cys Asn Asn Ser Cys Asp Ile Tyr Ile Leu Gly Phe Gln Glu Ile Val
      85      90      95
Pro Leu Lys Ala Ser Asn Val Leu Gly Ser Glu Asn Asn Glu Ile Ser
      100     105     110
Met Lys Trp Asn Ser Ile Ile Arg Glu Ala Leu Asn Lys Lys Ile Thr
      115     120     125
His Gln Arg Asp Lys Asp Ala Lys Lys Gln Glu Leu Lys Asn Asn Phe
      130     135     140
Pro Asn Lys Lys Glu Asn Pro Ala Lys Cys Cys Asp Ala Pro His Asp
      145     150     155     160
Phe Gln Cys Ile Ile Ser Lys Gln Met Val Gly Leu Phe Ile Ser Val
      165     170     175
Trp Ile Arg Arg Asp Leu Cys Pro Phe Ile Arg His Pro Ser Val Ser
      180     185     190
Cys Val Gly Cys Gly Ile Met Gly Cys Leu Gly Asn Lys Gly Ser Ile
      195     200     205
Ser Val Arg Phe Gln Leu His Glu Thr Ser Phe Cys Phe Val Cys Ser
      210     215     220
His Leu Ala Ser Gly Gly Arg Glu Gly Asp Glu Lys His Arg Asn Ser
      225     230     235     240
Asn Val Ala Glu Ile Phe Ser Arg Thr Ser Phe Pro Arg Gly Pro Leu
      245     250     255

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Leu	Asp	Leu	Pro	Arg	Thr	Ile	Leu	Asp	His	Asp	His	Val	Ile	Leu	Leu
			260					265					270		
Gly	Asp	Leu	Asn	Tyr	Arg	Ile	Ser	Leu	Pro	Glu	Glu	Thr	Thr	Arg	Leu
		275					280					285			
Leu	Val	Glu	Lys	Arg	Asp	Trp	Asp	Ser	Leu	Leu	Ala	Asn	Asp	Gln	Leu
		290				295					300				
Ile	Met	Glu	Leu	Met	Ser	Gly	Asn	Met	Leu	Arg	Gly	Trp	His	Glu	Gly
305					310					315				320	
Ala	Ile	Lys	Phe	Ala	Pro	Thr	Tyr	Lys	Tyr	Cys	Pro	Asn	Ser	Asp	Ile
			325						330					335	
Tyr	Tyr	Gly	Cys	Cys	Tyr	His	Gly	Lys	Lys	Ala	Glu	Lys	Arg	Arg	Ala
		340						345					350		
Pro	Ala	Trp	Cys	Asp	Arg	Ile	Val	Trp	Cys	Gly	Glu	Gly	Leu	Lys	Gln
		355					360					365			
Leu	Gln	Tyr	Thr	Arg	Ile	Glu	Ser	Lys	Leu	Ser	Asp	His	Arg	Pro	Val
	370					375					380				
Lys	Ala	Met	Phe	Ile	Ala	Glu	Val	Arg	Val	Leu	Pro	Glu	Leu	Met	Lys
385					390					395					400
Asn	Leu	Gln	Ser	Leu	Phe	Leu	Ser	Glu	Arg	Tyr	Glu	Gln	Ile	Lys	Thr
			405					410						415	
Pro	Phe	Glu	Val	Ser	Thr	Thr	Glu	Asp	Phe	Val	Asn	Arg	Lys	Arg	Ser
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Ser	Phe	Arg	Leu												
		435													

<210> 22

<211> 1600

<212> DNA

<213> Glycine max

<400> 22

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ataatttcta caaaaaaaaaa gttcgataaa ataagtagag aacgtgtatt aataatttct 180
acataagaaa taaagaaata tattagatat aataagtgat gcaagaaaga tggacaaaaa 240
taattacgta aatatcattc tataaattta ttattcatta tataaatagc attaccattg 300
ttgaaacttg aaagtgggtc catcgtttac aactaaagaa agacacccta gcgtaaaata 360
ttcaaccatc gacgtctact tcaattaaca tgaagatgta gttccatctc aacggatttc 420
cgtctcaaat aaaattctta ataacgtgct actaaccatt ggaatctgca gaatatctcg 480
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caagaacgtt tatatatata taattttact aaacaaatcg taatacaaaa ctttattatt 600
ataacgtgat ttgtcacttt ttgcttcaga aaaatacttt gtacaaaaa ttaagacaat 660
aacataagtt gccaatacca tacataaaac tctttaatga atcataatga tgaaaattga 720
gagatattta gttccatgat aaagagtgtg tttgtgtggg aatttgacca aacgcaattg 780
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gaaaaaaaga aaaagaaaaa acaagtcaca tattttattc ttatgtcagc caaaaacttg 1020
actagctgta gatggggcaa taataactag ctattcatca catttcctag ctaattgcct 1080
gttttgttat ggaccacatt cccacttgca ctcatcttca gcaatttaaa ttaggtaata 1140
aacattaaga tatcctttta aatctactca acaaacagaa gaattcaaat ctgcaagaag 1200
ggtagaccca tgtttttata tagctttctc tatctctctc ccactgggac ataaatgttc 1260
ctatatctca aaaaatatat atatgatatg atgagcaatg cagccaaagg tgcattcatc 1320
tttacgtcac atgaaagcct ttctacctc ttcaagctgc acaagccttt ctctttccca 1380
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 Asp Ile Ala Gly Lys Lys Leu Arg Thr Gly Ile Asp Tyr Tyr Ile Leu
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 Pro Val Val Arg Gly Arg Gly Gly Gly Leu Thr Leu Asp Ser Thr Gly
 50 55 60
 Asn Glu Ser Cys Pro Leu Asp Ala Val Val Gln Glu Gln Gln Glu Ile
 65 70 75 80
 Lys Asn Gly Leu Pro Leu Thr Phe Thr Pro Val Asn Pro Lys Lys Gly
 85 90 95
 Val Ile Arg Glu Ser Thr Asp Leu Asn Ile Lys Phe Ser Ala Ala Ser
 100 105 110
 Ile Cys Val Gln Thr Thr Leu Trp Lys Leu Asp Asp Phe Asp Glu Thr
 115 120 125
 Thr Gly Lys Tyr Phe Ile Thr Ile Gly Gly Asn Glu Gly Asn Pro Gly
 130 135 140
 Arg Glu Thr Ile Ser Asn Trp Phe Lys Ile Glu Lys Phe Glu Arg Asp
 145 150 155 160
 Tyr Lys Leu Val Tyr Cys Pro Thr Val Cys Asn Phe Cys Lys Val Ile
 165 170 175
 Cys Lys Asp Val Gly Ile Phe Ile Gln Asp Gly Ile Arg Arg Leu Ala
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 Lys Asp
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 35 40 45
 Gly Gly Ala Ala Ser Leu Ser Gln Ile Leu Ser Lys Val His Leu His
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 Pro Ser Arg Val Ser Ser Leu Arg Arg Leu Met Arg Val Leu Thr Thr
 65 70 75 80
 Thr Asn Val Phe Gly Thr Gln Pro Leu Gly Gly Gly Ser Asp Asp Asp
 85 90 95
 Ser Glu Pro Val Tyr Thr Leu Thr Pro Val Ser Arg Leu Leu Ile Gly
 100 105 110
 Ser Gln Ser Ser Gln Leu Ala Gln Thr Pro Leu Ala Ala Met Val Leu
 115 120 125

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His	Glu	Leu	Pro	Asp	Pro	Cys	Ile	Phe	Lys	His	Thr	His	Gly	Arg	Gly
145					150					155					160
Ile	Trp	Glu	Leu	Thr	Lys	Asp	Asp	Ala	Thr	Phe	Asp	Ala	Leu	Val	Asn
				165					170					175	
Asp	Gly	Leu	Ala	Ser	Asp	Ser	Gln	Leu	Ile	Val	Asp	Val	Ala	Ile	Lys
			180					185					190		
Gln	Ser	Ala	Glu	Val	Phe	Gln	Gly	Ile	Ser	Ser	Leu	Val	Asp	Val	Gly
		195					200					205			
Gly	Gly	Ile	Gly	Ala	Ala	Ala	Gln	Ala	Ile	Ser	Lys	Ala	Phe	Pro	His
	210					215					220				
Val	Lys	Cys	Ser	Val	Leu	Asp	Leu	Ala	His	Val	Val	Ala	Lys	Ala	Pro
225					230					235					240
Thr	His	Thr	Asp	Val	Gln	Phe	Ile	Ala	Gly	Asp	Met	Phe	Glu	Ser	Ile
				245					250					255	
Pro	Pro	Ala	Asp	Ala	Val	Leu	Leu	Lys	Ser	Val	Leu	His	Asp	Trp	Asp
			260					265					270		
His	Asp	Asp	Cys	Val	Lys	Ile	Leu	Lys	Asn	Cys	Lys	Lys	Ala	Ile	Pro
		275					280					285			
Pro	Arg	Glu	Ala	Gly	Gly	Lys	Val	Ile	Ile	Ile	Asn	Met	Val	Val	Gly
	290					295					300				
Ala	Gly	Pro	Ser	Asp	Met	Lys	His	Lys	Glu	Met	Gln	Ala	Ile	Phe	Asp
305					310					315					320
Val	Tyr	Ile	Met	Phe	Ile	Asn	Gly	Met	Glu	Arg	Asp	Glu	Gln	Glu	Trp
				325					330					335	
Ser	Lys	Ile	Phe	Ser	Glu	Ala	Gly	Tyr	Ser	Asp	Tyr	Arg	Ile	Ile	Pro
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<211> 352

<212> PRT

<213> Medicago sativa

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Leu	Lys	Trp	Ala	Val	Glu	Met	Asn	Ile	Pro	Asn	Ile	Ile	Gln	Asn	His
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Gly	Lys	Pro	Ile	Ser	Leu	Ser	Asn	Leu	Val	Ser	Ile	Leu	Gln	Val	Pro
	50					55					60				
Ser	Ser	Lys	Ile	Gly	Asn	Val	Arg	Arg	Leu	Met	Arg	Tyr	Leu	Ala	His
65					70					75				80	
Asn	Gly	Phe	Phe	Glu	Ile	Ile	Thr	Lys	Glu	Glu	Glu	Ser	Tyr	Ala	Leu
			85						90					95	
Thr	Val	Ala	Ser	Glu	Leu	Leu	Val	Arg	Gly	Ser	Asp	Leu	Cys	Leu	Ala
		100						105					110		
Pro	Met	Val	Glu	Cys	Val	Leu	Asp	Pro	Thr	Leu	Ser	Gly	Ser	Tyr	His
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Glu	Leu	Lys	Lys	Trp	Ile	Tyr	Glu	Glu	Asp	Leu	Thr	Leu	Phe	Gly	Val
	130					135					140				
Thr	Leu	Gly	Ser	Gly	Phe	Trp	Asp	Phe	Leu	Asp	Lys	Asn	Pro	Glu	Tyr
145					150					155					160

Asn	Thr	Ser	Phe	Asn	Asp	Ala	Met	Ala	Ser	Asp	Ser	Lys	Leu	Ile	Asn	
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Leu	Ala	Leu	Arg	Asp	Cys	Asp	Phe	Val	Phe	Asp	Gly	Leu	Glu	Ser	Ile	
			180					185					190			
Val	Asp	Val	Gly	Gly	Gly	Thr	Gly	Thr	Thr	Ala	Lys	Ile	Ile	Cys	Glu	
	195						200					205				
Thr	Phe	Pro	Lys	Leu	Lys	Cys	Ile	Val	Phe	Asp	Arg	Pro	Gln	Val	Val	
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Glu	Asn	Leu	Ser	Gly	Ser	Asn	Asn	Leu	Thr	Tyr	Val	Gly	Gly	Asp	Met	
225					230					235					240	
Phe	Thr	Ser	Ile	Pro	Asn	Ala	Asp	Ala	Val	Leu	Leu	Lys	Tyr	Ile	Leu	
			245						250					255		
His	Asn	Trp	Thr	Asp	Lys	Asp	Cys	Leu	Arg	Ile	Leu	Lys	Lys	Cys	Lys	
			260					265					270			
Glu	Ala	Val	Thr	Asn	Asp	Gly	Lys	Arg	Gly	Lys	Val	Thr	Ile	Ile	Asp	
	275						280					285				
Met	Val	Ile	Asp	Glu	Lys	Lys	Asp	Glu	Asn	Gln	Val	Thr	Gln	Ile	Lys	
	290					295					300					
Leu	Leu	Met	Asp	Val	Asn	Met	Ala	Cys	Leu	Asn	Gly	Lys	Glu	Arg	Asn	
305					310					315					320	
Glu	Glu	Glu	Trp	Lys	Lys	Leu	Phe	Ile	Glu	Ala	Gly	Phe	Gln	His	Tyr	
			325					330					335			
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<211> 664

<212> PRT

<213> Arabidopsis thaliana

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			20					25					30			
Ile	Ser	Gly	Arg	Asp	Pro	Glu	Tyr	Gly	Ala	Asp	Thr	Asp	Asn	Glu	Ser	
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Glu	Asn	Glu	Asp	Ala	Arg	Glu	Asp	Asn	Asp	Asp	Ser	Ser	Ser	Asp	Glu	
	50					55					60					
Glu	Gly	Gly	Ser	Gly	Ser	Arg	Gly	Arg	Glu	Ser	Lys	Val	Tyr	Glu	Asn	
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Ala	Glu	Asp	Ala	Ile	Ala	Ala	Ala	Ser	Ala	Val	Val	Asp	Ala	Ala	Ala	
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	130					135					140					
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Tyr	Val	Leu	Gly	Ser	Gln	Glu	Ile	Val	Pro	Leu	Asn	Ala	Gly	Asn	Ile	
			165					170						175		
Leu	Gly	Ala	Glu	Asp	Asp	Arg	Pro	Val	Ala	Lys	Trp	Glu	Glu	Val	Ile	
			180					185					190			
Arg	Glu	Ala	Leu	Asn	Arg	Val	Arg	Pro	Lys	Leu	Ser	Gly	Val	Lys	Ser	
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Gly	Val	Glu	Ile	His	Pro	Ile	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Thr	Asp
				245						250					255
Arg	Leu	Trp	Ala	Leu	Lys	His	Asp	Gly	Gly	Val	Ile	Gly	Glu	Val	Lys
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Thr	Leu	Val	Asp	Pro	Asn	Thr	Gly	Leu	Pro	Val	Val	Glu	Ile	Lys	Arg
		275					280					285			
Gln	Phe	Ser	Ile	Pro	Lys	Lys	Leu	Asp	Arg	Gln	Leu	Cys	Leu	Arg	Ala
	290					295					300				
Asp	Ser	Phe	Lys	Gly	Ile	Ser	Asp	Asp	Asp	Ser	Thr	Gln	Thr	Gly	Met
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Lys	Thr	Ile	Asn	Arg	Met	Leu	Ser	Gly	Lys	Glu	Arg	Ile	Gly	Leu	Ser
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Trp	Pro	Glu	Pro	Pro	Leu	Asn	Met	Leu	Gly	Pro	Cys	Val	Leu	Asp	Arg
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Gln	Pro	Ser	Ile	Lys	Thr	Val	Lys	Ser	Leu	Lys	Thr	Ala	Lys	Ser	Phe
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Lys	Ala	Tyr	Ser	Ser	Phe	Lys	Ser	Val	Ala	Gly	Asn	Asn	Asn	Gly	Ile
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Pro	Pro	Glu	Val	Leu	Ala	Leu	Ala	Glu	Met	Asp	Leu	Lys	Leu	Leu	Met
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Glu	Arg	Lys	Arg	Arg	Pro	Ala	Tyr	Val	Arg	Leu	Val	Ser	Lys	Gln	Met
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Val	Gly	Ile	Leu	Leu	Thr	Ile	Trp	Val	Lys	Arg	Ser	Leu	Arg	Lys	His
			420					425					430		
Ile	Gln	Asn	Val	Arg	Val	Ser	Thr	Val	Gly	Val	Gly	Val	Met	Gly	Tyr
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Ile	Gly	Asn	Lys	Gly	Ala	Val	Ser	Val	Ser	Met	Ser	Ile	Asn	Gln	Thr
	450					455					460				
Phe	Phe	Cys	Phe	Ile	Asn	Thr	His	Leu	Thr	Ala	Gly	Glu	Arg	Glu	Val
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Asp	Gln	Ile	Lys	Arg	Asn	Ala	Asp	Val	His	Glu	Ile	His	Lys	Arg	Thr
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Val	Phe	His	Ser	Val	Ser	Ala	Leu	Gly	Leu	Pro	Lys	Leu	Ile	Tyr	Asp
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His	Glu	Arg	Ile	Ile	Trp	Leu	Gly	Asp	Leu	Asn	Tyr	Arg	Leu	Ser	Ser
		515					520					525			
Ser	Tyr	Glu	Lys	Thr	Arg	Asp	Leu	Ile	Ser	Lys	Arg	Glu	Trp	Ser	Lys
	530					535					540				
Leu	Leu	Glu	Tyr	Asp	Gln	Leu	Val	Lys	Glu	Tyr	Arg	Lys	Gly	Arg	Ala
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Phe	Asp	Gly	Trp	Ser	Glu	Gly	Thr	Leu	His	Phe	Pro	Pro	Thr	Tyr	Lys
				565					570					575	
Tyr	Gln	Ala	Asn	Ser	Asp	Glu	Tyr	Thr	Ala	Asn	Asp	Gly	Lys	Ala	Pro
			580					585					590		
Lys	Arg	Thr	Pro	Ala	Trp	Cys	Asp	Arg	Val	Leu	Ser	Tyr	Gly	Lys	Gly
		595					600					605			
Met	Arg	Leu	Val	His	Tyr	Arg	Arg	Thr	Glu	Gln	Lys	Phe	Ser	Asp	His
	610					615					620				
Arg	Pro	Val	Thr	Ala	Ile	Tyr	Met	Ala	Glu	Val	Glu	Val	Phe	Ser	Ala
625					630					635					640
Arg	Lys	Leu	Gln	Arg	Ala	Leu	Thr	Phe	Thr	Asp	Ala	Glu	Ile	Glu	Asp
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 35 40 45
 His Pro Thr Asn Gln Val Asn Val Lys Glu Glu Glu Ala Val Lys Lys
 50 55 60
 Glu Gln Ala Thr Glu Pro Gly Lys Arg Arg Lys Arg Lys Asn Val Tyr
 65 70 75 80
 Arg Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg
 85 90 95
 Asp Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr Ala
 100 105 110
 Glu Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys Gln Ile Arg Gly
 115 120 125
 Glu Lys Ala Lys Leu Asn Phe Pro Asp Leu Asp His His Pro Ser Thr
 130 135 140
 Pro Pro Pro Ser Ser Thr Ser Leu Arg Leu Ser Asp Gln Pro Pro Ala
 145 150 155 160
 Lys Lys Val Cys Val Val Ser Gln Ser Glu Leu Ala Gln Pro Ser Phe
 165 170 175
 Pro Val Glu Cys Val Gly Phe Gly Lys Gly Glu Glu Phe Gln Asn Leu
 180 185 190
 Met Tyr Gly Phe Glu Pro Asp Tyr Asp Leu Lys Gln Gln Ile Ser Ser
 195 200 205
 Leu Glu Ser Phe Leu Glu Leu Asp Gly Thr Thr Ala Glu Gln Pro Ser
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 Val Ile Ala Ser Tyr Glu

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 35 40 45
 His Pro Thr Asn Gln Val Asn Val Lys Glu Glu Ala Val Lys Lys Glu
 50 55 60
 Gln Ala Thr Glu Pro Gly Lys Arg Arg Lys Arg Lys Asn Val Tyr Arg
 65 70 75 80
 Gly Ile Arg Lys Arg Pro Trp Gly Lys Trp Ala Ala Glu Ile Arg Asp
 85 90 95
 Pro Arg Lys Gly Val Arg Val Trp Leu Gly Thr Phe Asn Thr Ala Glu
 100 105 110
 Glu Ala Ala Met Ala Tyr Asp Val Ala Ala Lys Gln Ile Arg Gly Asp
 115 120 125
 Lys Ala Lys Leu Asn Phe Pro Asp Leu His His Pro Pro Pro Pro Asn
 130 135 140
 Tyr Thr Pro Pro Pro Ser Ser Pro Arg Ser Thr Asp Gln Pro Pro Ala
 145 150 155 160
 Lys Lys Val Cys Val Val Ser Gln Ser Glu Ser Glu Leu Ser Gln Pro
 165 170 175
 Ser Phe Pro Val Glu Cys Ile Gly Phe Gly Asn Gly Asp Glu Phe Gln
 180 185 190
 Asn Leu Ser Tyr Gly Phe Glu Pro Asp Tyr Asp Leu Lys Gln Gln Ile
 195 200 205
 Ser Ser Leu Glu Ser Phe Leu Glu Leu Asp Gly Asn Thr Ala Glu Gln
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Gln	Lys	Ser	Ala	Pro	His	Arg	Asp	Phe	Tyr	Asn	Val	Arg	Lys	Val	Asp	
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act	cat	gtc	cac	cac	tca	gca	tgc	atg	aat	cag	aaa	cat	ctt	tta	agg	149
Thr	His	Val	His	His	Ser	Ala	Cys	Met	Asn	Gln	Lys	His	Leu	Leu	Arg	
			30					35					40			
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Phe	Ile	Lys	Ser	Lys	Leu	Arg	Lys	Glu	Pro	Asp	Glu	Val	Val	Ile	Phe	
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cga	gat	ggg	aca	tat	cta	acg	ttg	gaa	gag	ggt	ttc	aag	agt	tta	gat	245
Arg	Asp	Gly	Thr	Tyr	Leu	Thr	Leu	Glu	Glu	Val	Phe	Lys	Ser	Leu	Asp	
	60					65					70					
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Leu	Ser	Gly	Tyr	Asp	Leu	Asn	Val	Asp	Leu	Leu	Asp	Val	His	Ala	Asp	
75					80				85						90	
aag	agt	act	ttt	cat	cgc	ttt	gat	aag	ttc	aat	ctt	aaa	tac	aat	cct	341
Lys	Ser	Thr	Phe	His	Arg	Phe	Asp	Lys	Phe	Asn	Leu	Lys	Tyr	Asn	Pro	
				95					100					105		
tgc	ggt	caa	agt	agg	ctc	agg	gag	ata	ttt	ctt	aag	cag	gat	aat	ctc	389
Cys	Gly	Gln	Ser	Arg	Leu	Arg	Glu	Ile	Phe	Leu	Lys	Gln	Asp	Asn	Leu	
			110					115					120			
att	caa	ggt	cgt	ttt	ctt	ggt	gag	tta	act	aag	caa	gtg	ttt	tca	gat	437
Ile	Gln	Gly	Arg	Phe	Leu	Gly	Glu	Leu	Thr	Lys	Gln	Val	Phe	Ser	Asp	
		125					130					135				
ctt	gct	gcc	agt	aaa	tat	cag	atg	gct	gaa	tat	aga	ata	tca	ata	tat	485
Leu	Ala	Ala	Ser	Lys	Tyr	Gln	Met	Ala	Glu	Tyr	Arg	Ile	Ser	Ile	Tyr	
	140					145					150					
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Gly	Arg	Lys	Gln	Ser	Glu	Trp	Asp	Gln	Leu	Ala	Ser	Trp	Ile	Val	Asn	
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Asn	Asp	Leu	Tyr	Ser	Glu	Asn	Val	Val	Trp	Leu	Ile	Gln	Leu	Pro	Arg	
				175					180					185		
ttg	tac	aat	gtg	tac	aaa	gaa	atg	gga	att	gtg	aca	tca	ttc	cag	aac	629
Leu	Tyr	Asn	Val	Tyr	Lys	Glu	Met	Gly	Ile	Val	Thr	Ser	Phe	Gln	Asn	
			190					195					200			
atg	ctc	gac	aat	att	ttc	att	cca	ctt	ttt	gag	gtc	act	gtc	aac	cca	677
Met	Leu	Asp	Asn	Ile	Phe	Ile	Pro	Leu	Phe	Glu	Val	Thr	Val	Asn	Pro	
		205					210					215				
gat	tca	cat	cct	cag	ctg	cat	gtt	ttc	ctg	aaa	cag	gtt	gtt	ggg	ttg	725
Asp	Ser	His	Pro	Gln	Leu	His	Val	Phe	Leu	Lys	Gln	Val	Val	Gly	Leu	
	220					225					230					
gat	ttg	gtt	gat	gat	gaa	agc	aaa	cct	gaa	aga	cgg	cca	aca	aaa	cac	773
Asp	Leu	Val	Asp	Asp	Glu	Ser	Lys	Pro	Glu	Arg	Arg	Pro	Thr	Lys	His	
235					240					245					250	

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Met Pro Thr Pro Glu Gln Trp Thr Asn Val Phe Asn Pro Ala Phe Ser	
255 260 265	
tac tat gtc tat tac tgt tat gca aat ctt tac acc tta aac aag ctt	869
Tyr Tyr Val Tyr Tyr Cys Tyr Ala Asn Leu Tyr Thr Leu Asn Lys Leu	
270 275 280	
cga gaa tca aag gga atg aca aca atc aaa ttc cgt cca cat tct gga	917
Arg Glu Ser Lys Gly Met Thr Thr Ile Lys Phe Arg Pro His Ser Gly	
285 290 295	
gag gct ggt gat att gac cac ctt gca gca acc ttt ctc acg gct cac	965
Glu Ala Gly Asp Ile Asp His Leu Ala Ala Thr Phe Leu Thr Ala His	
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aac att gca cat gga atc aat ttg aaa aaa tct cct gtg ctt caa tat	1013
Asn Ile Ala His Gly Ile Asn Leu Lys Lys Ser Pro Val Leu Gln Tyr	
315 320 325 330	
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Leu Tyr Tyr Leu Ala Gln Ile Gly Leu Ala Met Ser Pro Leu Ser Asn	
335 340 345	
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Asn Ser Leu Phe Leu Asp Tyr His Arg Asn Pro Phe Pro Met Phe Phe	
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tta cgg ggt ctg aat gtg tca ctt tct act gat gat cct ctc caa att	1157
Leu Arg Gly Leu Asn Val Ser Leu Ser Thr Asp Asp Pro Leu Gln Ile	
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His Leu Thr Lys Glu Pro Leu Val Glu Glu Tyr Ser Ile Ala Ala Ser	
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Val Trp Lys Leu Ser Ser Cys Asp Leu Cys Glu Ile Ala Arg Asn Ser	
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Val Tyr Gln Ser Gly Phe Ser His Ala Leu Lys Ser His Trp Ile Gly	
415 420 425	
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Lys Glu Tyr Tyr Lys Ser Gly Pro Arg Gly Asn Asp Ile Gln Arg Thr	
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Asn Val Pro His Ile Arg Leu Glu Phe Arg Asp Thr Ile Trp Arg Glu	
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Glu Met Gln Gln Val Tyr Leu Gly Lys Ala Ile Ile Pro Glu Val Val	
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Asp Lys *
475

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<212> PRT

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Ala Cys Met Asn Gln Lys His Leu Leu Arg Phe Ile Lys Ser Lys Leu
      35           40           45
Arg Lys Glu Pro Asp Glu Val Val Ile Phe Arg Asp Gly Thr Tyr Leu
      50           55           60
Thr Leu Glu Glu Val Phe Lys Ser Leu Asp Leu Ser Gly Tyr Asp Leu
      65           70           75           80
Asn Val Asp Leu Leu Asp Val His Ala Asp Lys Ser Thr Phe His Arg
      85           90           95
Phe Asp Lys Phe Asn Leu Lys Tyr Asn Pro Cys Gly Gln Ser Arg Leu
      100          105          110
Arg Glu Ile Phe Leu Lys Gln Asp Asn Leu Ile Gln Gly Arg Phe Leu
      115          120          125
Gly Glu Leu Thr Lys Gln Val Phe Ser Asp Leu Ala Ala Ser Lys Tyr
      130          135          140
Gln Met Ala Glu Tyr Arg Ile Ser Ile Tyr Gly Arg Lys Gln Ser Glu
      145          150          155          160
Trp Asp Gln Leu Ala Ser Trp Ile Val Asn Asn Asp Leu Tyr Ser Glu
      165          170          175
Asn Val Val Trp Leu Ile Gln Leu Pro Arg Leu Tyr Asn Val Tyr Lys
      180          185          190
Glu Met Gly Ile Val Thr Ser Phe Gln Asn Met Leu Asp Asn Ile Phe
      195          200          205
Ile Pro Leu Phe Glu Val Thr Val Asn Pro Asp Ser His Pro Gln Leu
      210          215          220
His Val Phe Leu Lys Gln Val Val Gly Leu Asp Leu Val Asp Asp Glu
      225          230          235          240
Ser Lys Pro Glu Arg Arg Pro Thr Lys His Met Pro Thr Pro Glu Gln
      245          250          255
Trp Thr Asn Val Phe Asn Pro Ala Phe Ser Tyr Tyr Val Tyr Tyr Cys
      260          265          270
Tyr Ala Asn Leu Tyr Thr Leu Asn Lys Leu Arg Glu Ser Lys Gly Met
      275          280          285
Thr Thr Ile Lys Phe Arg Pro His Ser Gly Glu Ala Gly Asp Ile Asp
      290          295          300
His Leu Ala Ala Thr Phe Leu Thr Ala His Asn Ile Ala His Gly Ile
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Asn Leu Lys Lys Ser Pro Val Leu Gln Tyr Leu Tyr Tyr Leu Ala Gln
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Ile	Gly	Leu	Ala	Met	Ser	Pro	Leu	Ser	Asn	Asn	Ser	Leu	Phe	Leu	Asp	
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Tyr	His	Arg	Asn	Pro	Phe	Pro	Met	Phe	Phe	Leu	Arg	Gly	Leu	Asn	Val	
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Leu	Val	Glu	Glu	Tyr	Ser	Ile	Ala	Ala	Ser	Val	Trp	Lys	Leu	Ser	Ser	
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Cys	Asp	Leu	Cys	Glu	Ile	Ala	Arg	Asn	Ser	Val	Tyr	Gln	Ser	Gly	Phe	
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Ser	His	Ala	Leu	Lys	Ser	His	Trp	Ile	Gly	Lys	Glu	Tyr	Tyr	Lys	Ser	
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Gly	Pro	Arg	Gly	Asn	Asp	Ile	Gln	Arg	Thr	Asn	Val	Pro	His	Ile	Arg	
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Leu	Glu	Phe	Arg	Asp	Thr	Ile	Trp	Arg	Glu	Glu	Met	Gln	Gln	Val	Tyr	
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Leu	Gly	Lys	Ala	Ile	Ile	Pro	Glu	Val	Val	Asp	Lys					
465					470					475						